AMENDMENTS

44. (Previously presented) A method for identifying a population of bi-ligands to dehydrogenases in a dehdrogenase enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of a dehydrogenase in said dehydrogenase enzyme family, to form a module;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to a dehydrogenase in said dehydrogenase enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said dehydrogenase; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second dehydrogenase in said dehydrogenase enzyme family.

45. (Previously presented) The method of claim 44, wherein said expansion linker has approximate C2 symmetry.

46. (Previously presented) The method of claim 44, wherein said expansion linker has perfect C2 symmetry.

47. (Previously presented) A method for identifying a population of bi-ligands to enzymes in an enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of an enzyme in said enzyme family, to form a module, wherein said enzyme family binds the cofactor nicotinamide adenine dinucleotide or nicotinamide adenine dinucleotide phosphate;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to an enzyme in said enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said enzyme; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second enzyme in said enzyme family.

48. (Previously presented) The method of claim 47, wherein said enzyme family binds nicotinamide adenine dinucleotide.

49. (Previously presented) The method of claim 47, wherein said enzyme family binds nicotinamide adenine dinucleotide phosphate.

50. (Previously presented) The method of claim 47, wherein said expansion linker has approximate C2 symmetry.

51. (Previously presented) The method of claim 47, wherein said expansion linker has perfect C2 symmetry.

52. (Previously presented) A method for identifying a population of bi-ligands to dehydrogenases in a dehdrogenase enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of a dehydrogenase in said dehydrogenase enzyme family, to form a module, wherein said enzyme family binds the cofactor nicotinamide adenine dinucleotide or nicotinamide adenine dinucleotide phosphate;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to a dehydrogenase in said dehydrogenase enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said dehydrogenase; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second dehydrogenase in said dehydrogenase enzyme family.

53. (Previously presented) The method of claim 52, wherein said enzyme family binds nicotinamide adenine dinucleotide.

54. (Previously presented) The method of claim 52, wherein said enzyme family binds nicotinamide adenine dinucleotide phosphate.

55. (Previously presented) The method of claim 52, wherein said expansion linker has approximate C2 symmetry.

56. (Previously presented) The method of claim 52, wherein said expansion linker has perfect C2 symmetry.

Please add the following new claims.

57. (New) A method for identifying a population of bi-ligands to dehydrogenases in a dehdrogenase enzyme family, comprising:

(a) attaching a linker to a common ligand, wherein said common ligand is the cofactor nicotinamide adenine dinucleotide or nicotinamide adenine dinucleotide phosphate, or a mimic of said cofactor, and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of a dehydrogenase in said dehydrogenase enzyme family, to form a module;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to a dehydrogenase in said dehydrogenase enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said dehydrogenase; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second dehydrogenase in said dehydrogenase enzyme family.

58. (New) The method of claim 57, wherein said expansion linker has approximate C2 symmetry.

59. (New) The method of claim 57, wherein said expansion linker has perfect C2 symmetry.